

1 AATGGATTGG ACTCCGGTGG GGAAAGCGGG TGTCTAGAAG TGGTGCTAAT
 51 GGGAAAGAGAA TTCTGGTTTC AAAAGAGGAT GCTCTGCCAC AAAGAGCGGC
 101 TCGCGCGCTG GCCTGGGCTC TAGCCGAGGA GAGATCCCGG GAGAACTCCA
 151 GAGCTCCGGG GGAGCGCTCC TCGGAAGACCC GGGGCCAACA TGCCTGTGCG
 201 CAGGGGGCAT GTGGCACCC AAAATACATT TCTGGGGACC ATCATTCCGA
 251 AATTGAAAG GCAAAATAAA AAATTATCA TTGCAAATGC CAGAGTGCAG
 301 AACTGTGCCA TCATTTATTG CAACGATGGG TTCTGTGAGA TGACTGGTTT
 351 CTCCAGGCCA GATGTCATGC AAAAGCCATG CACCTGCGAC TTTCTCCATG
 401 GACCCGAGAC CAAGGGCAT GATATTGCCA AAATTGCCA GGCATTGCTG
 451 GGGTCAGAAG AGAGGAAAGT GGAGGTCACT TACTATCACA AAAATGGTC
 501 CACTTTATTG TGTAACACTC ACATAATTCC AGTAAAAAC CAAGAGGGCG
 551 TGGCTATGAT GTTCATCATT AATTGAAAT ATGTGACGGA TAATGAAAAC
 601 GCTGCCACCC CAGAGGGGT AAACCCAATA TTACCAATCA AAACGTAA
 651 CCGGAAATTG TTTGGGTTCA AATTCCCTGG TCTGAGACTT CTCACTTACA
 701 GAAAGCAGTC CTTACCACAA GAAGACCCCG ATGGTGGTGGT CATCGATTCA
 751 TCTAAACACA GTGATGATTG AGTAGCCATG AAGCATTAA AGTCTCTAC
 801 AAAAGAAAGC TGCAAGCCCT CTGAAGCAGA TGACACAAAA GCTTTGATAC
 851 AGCCCAGCAA ATGTTCTCCC TTGGTGAATA TATCCGGACC TCTTGACCAT
 901 TCCTCTCCCA AAAGGCAATG GGACCGACTC TACCCGTGACA TGCTGCAGTC
 951 AAGTTCCAG CTGTCCTCATT CCAGATCAAG GGAAGCTTA TGTAGTATAC
 1001 GGAGAGCATC TTGGTCCAT GATATAGAAG GATTGGCGT CCACCCCAAG
 1051 AACATATTCA GAGACCGACA TGCCAGCGAA GACAATGGTC GCAATGTCAA
 1101 AGTTTACAGT TCCTGGATGG CAGGGGGGCC TTTTAATCAT ATCAAGTCAA
 1151 GCCTCCTGGG ATCCACATCA GATTCAAACCC TCAACAAATA CAGCACCATT
 1201 ACAAGATTTC CACAGCTCAC TCTGAATTTC TCAGAGGTCA AAACGTAGAA
 1251 AAAGAATTCA TCACCTCCTT CTTCAGATAA AACCATTATT GCACCCCAAGG
 1301 TTAAAGATCG AACACACAAT GTGACTGAGA AAGTGCACCA GGTTCTCT
 1351 TTAGGAGCAG ATGTCCTACC TGAATACAAA CTGCAGACAC CACGCATCAA
 1401 CAAGTTTACG ATATTGCACT ACAGCCCTT CAAGGCAGTC TGGGACTGGC
 1451 TTATCCTGCT GTTGGTCATA TACACTGCTA TATTTACTCC CTACTCTGCA
 1501 GCCTTCCTCC TCAATGACAG AGAAGAACAG AAAAGACGAG AATGTGGCTA
 1551 TTCTTGTAGC CCTTTGAATG TGGTAGACTT GATTGTGGAT ATTATGTTA
 1601 TCATAGATAT TTTAATAAAC TTCAGAACAA CATATGTAAA TCAGAATGAA
 1651 GAAGTGGTAA GTGATCCCGC CAAAATAGCA ATACACTACT TCAAAGGCTG
 1701 GTTCCCTGATT GACATGGTTG CAGCAATTCC TTTTGACTTG CTGATTTTG
 1751 GATCAGGTTC TGATGAGGTA AGAACTGCTT AAGATTCTTA TTTTCTGAAA
 1801 GATTGCAATT ATAAAAAGTGA ATCTATTAA ACTGCAAAAAA GAAGAGTTGC
 1851 TTTGCAAGCT TCTTGATATCT CACTGATAAA ATTCATTTTC AATTGGGGAT
 1901 ACTACAGAAAT GAAATGAAAC CATTGGCCA TTGCAAATCA AATTCTTCT
 1951 CTTTTTGCTA AGAGATGCCA AAGATTCTCC ATTCCTTACC CACCAAAATT
 2001 AACATTGGAAA CAAAGTGGTCC ATAGCACACA GCACATTCCC AGGATTAAA
 2051 ATCTCTACTT ATTAACCTCA CGGGTGTAAA ACTCTCAAAT ATTAAGTATG
 2101 TCTCTGTTT TCTTAACCTCA TTGTTAAGGG TTGAGACAG CAGAGATTG
 2151 GTTTTTTGT TCAAATTATT GTGAAGAGGG CCCCCCTTCC GAAAT (SEQ ID NO:1)

FEATURES:

5'UTR: 1-189
 Start Codon: 190
 Stop Codon: 1780
 3'UTR: 1783

HOMOLOGOUS PROTEINS:

Top 10 BLAST Hits:

	Score	E
CRA 113000007753533 /altid=gi 4104136 /def=gb AAD01946.1 (AF03...	1058	0.0
CRA 36000087530063 /altid=gi 11121258 /def=emb CAC14797.1 (AJ2...	1041	0.0
CRA 18000005124020 /altid=gi 2745727 /def=gb AAB94741.1 (AF016...	1039	0.0
CRA 18000005107889 /altid=gi 7305203 /def=ref NP_038597.1 pota...	592	e-168
CRA 18000005107891 /altid=gi 2582015 /def=gb AAC53420.1 (AF012...	591	e-168
CRA 18000005084931 /altid=gi 2190505 /def=emb CAB09536.1 (Z961...	589	e-167
CRA 18000004922641 /altid=gi 4557729 /def=ref NP_000229.1 pota...	580	e-164
CRA 108000024648805 /altid=gi 12733048 /def=ref XP_004743.2 po...	580	e-164
CRA 164000136746223 /altid=gi 11933152 /def=dbj BAB19682.1 (AB...	580	e-164
CRA 1000737074349 /altid=gi 6687230 /def=emb CAB64868.1 (AJ243...	570	e-161

BLAST dbEST hit:

gi|2229460 /dataset=dbest /taxon=9606 ... 434 e-119

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hit:

gi|2229460 testis

From tissue screening panels:

whole_brain

1 MPVRRGHVAP QNTFLGTIIR KFEGQNKFI IANARVQNC A IIYCNDGFCE
51 MTGFSRPDVM QKPCTCDFLH GPETKRHDIA QIAQALLGSE ERKVEVTTYH
101 KNGSTFICNT HIIIPVKNQEG VAMMFIINFE YVTDNENAAT PERVNPILPI
151 KTVNRKFFGF KFPGLRLLTY RKQSLPQEDP DVVVIDSSKH SDDSVAMKHF
201 KSPTKESCSP SEADDTKALI QPSKCSPLVN ISGPLDHSSP KRQWDRLYPD
251 MLQSSSQLSH SRSRESLCSI RRASSVHDIE GFGVHPKNIF RDRHASEDNG
301 RNVKVSRSWM AGGPFNHIKS SLLGSTSDSN LNKYSTINKI PQTLNFSFV
351 KTEKKNSSPP SSDKTIAPK VKDRTHNVTE KVTQVLSLGA DVLPEYKLQT
401 PRINKFTILH YSPFKAVVWDW LILLLVIYTA IFTPYSAAFL LNDREEQKRR
451 ECGYSCSPLN VVDLIVDIMP IIDILINFRT TYVNQNEEVV SDPAKIAIHY
501 FKGWFLIDMV AAIPFDLLIF GSGSDEVRTA (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

Number of matches: 4

1	102-105	NGST
2	230-233	NISG
3	346-349	NFSE
4	377-380	NVTE

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

CAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 3

1	171-174	RKQS
2	271-274	RRAS
3	354-357	KKNS

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 9

1	74-76	TKR
2	169-171	TYR
3	187-189	SSK
4	239-241	SPK
5	269-271	SIR
6	352-354	TEK
7	379-381	TEK
8	362-364	SDK
9	352-354	TEK

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 7

1	55-58	SRPD
2	133-136	TDNE
3	209-212	SPSE
4	211-214	SEAD
5	275-278	SVHD
6	325-328	STSD
7	522-525	SGSD

[5] PDOC00007 PS00007 TYR PHOSPHO SITE
Tyrosine kinase phosphorylation site

Number of matches: 3
1 92-99 RKVEVTYY
2 241-248 KRQWDRLY
3 448-454 KRRECGY

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

312-317 GGPFNH

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	420	440	1.885	Certain
2	504	524	1.071	Certain

BLAST Alignment to Top Hit:

>CRA|113000007753533 /altid=gi|4104136 /def=gb|AAD01946.1|
 (AF032897) potassium channel subunit [Homo sapiens]
 /org=Homo sapiens /taxon=9606 /dataset=nraa /length=1196
 Length = 1196

Score = 1058 bits (2705), Expect = 0.0
 Identities = 518/529 (97%), Positives = 519/529 (97%), Gaps = 8/529 (1%)

Query: 1 MPVRRGHVAPQNTFLGTIIRKFEQNKFFIANARVQNCIIYCNDGCEMTGFSRPDVM 60
 MPVRRGHVAPQNTFLGTIIRKFEQNKFFIANARVQNCIIYCNDGCEMTGFSRPDVM
 Sbjct: 1 MPVRRGHVAPQNTFLGTIIRKFEQNKFFIANARVQNCIIYCNDGCEMTGFSRPDVM 60

Query: 61 QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTYYHKNGSTFICNTHIIPVKNQEG 120
 QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTYYHKNGSTFICNTHIIPVKNQEG
 Sbjct: 61 QKPCTCDFLHGPETKRHDIAQIAQALLGSEERKVEVTYYHKNGSTFICNTHIIPVKNQEG 120

Query: 121 VAMMFIIINFYVTDNENAATPERVNPILPIKTVNRKFFGFKFPGLRLLTYRKQSLPQEDP 180
 VAMMFIIINFYVTDNENAATPERVNPILPIKTVNRKFFGFKFPGLR+LTYRKQSLPQEDP
 Sbjct: 121 VAMMFIIINFYVTDNENAATPERVNPILPIKTVNRKFFGFKFPGLRVLTYRKQSLPQEDP 180

Query: 181 DVVIDSSKHSDDSVAMKHFKSPKESCPSEADDTKALIQPSKCSPLVNISGPLDHSSP 240
 DVVIDSSKHSDDSVAMKHFKSPKESCPSEADDTKALIQPSKCSPLVNISGPLDHSSP
 Sbjct: 181 DVVIDSSKHSDDSVAMKHFKSPKESCPSEADDTKALIQPSKCSPLVNISGPLDHSSP 240

Query: 241 KRWDRILYPDMLQSSSQLSHSRSLCSIRRASSVHDIEGFGVHPKNIFRDRHASEDNG 300
 KRWDRILYPDMLQSSSQLSHSRSLCSIRRASSVHDIEGFGVHPKNIFRDRHASEDNG
 Sbjct: 241 KRWDRILYPDMLQSSSQLSHSRSLCSIRRASSVHDIEGFGVHPKNIFRDRHASEDNG 300

Query: 301 RNVKVSRSWMAAGPFNHIKSSLIGSTSDSLNLKYSTINKIPQLTLNFSEVKTEKKNSSPP 360
 RNVK GPFNHIKSSLIGSTSDSLNLKYSTINKIPQLTLNFSEVKTEKKNSSPP
 Sbjct: 301 RNVK-----GPFNHIKSSLIGSTSDSLNLKYSTINKIPQLTLNFSEVKTEKKNSSPP 352

Query: 361 SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLOTPRINKFTILHYSPEFKAVWDW 420
 SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLOTPRINKFTILHYSPEFKAVWDW
 Sbjct: 353 SSDKTIIAPKVKDRTHNVTEKVTQVLSLGADVLPEYKLOTPRINKFTILHYSPEFKAVWDW 412

Query: 421 LLLLVIYTAIFTPYSAAFLLNDREEQKRRECGYSCSPLNVDLIVDIMFIIDILINFRT 480
 LLLLVIYTAIFTPYSAAFLLNDREEQKRRECGYSCSPLNVDLIVDIMFIIDILINFRT
 Sbjct: 413 LLLLVIYTAIFTPYSAAFLLNDREEQKRRECGYSCSPLNVDLIVDIMFIIDILINFRT 472

Query: 481 TYVNQNEEVVSDPAKIAIHYFKGWFLIDMVAAPFDLIFGSGSDEVRT 529
 TYVNQNEEVVSDPAKIAIHYFKGWFLIDMVAAPFDLIFGSGSDE T
 Sbjct: 473 TYVNQNEEVVSDPAKIAIHYFKGWFLIDMVAAPFDLIFGSGSDETTT 521 (SEQ ID NO:4)

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00914	Transmembrane region cyclic Nucleotide Gated	34.2	1.4e-08	1
CE00367	E00367 brain_cyclic_nucleotide_gated_channel	30.3	5.1e-08	1
PF00785	PAC motif	16.2	0.006	1
PF00989	PAS domain	6.4	3.7	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00989	1/1	41	60 ..	26	45 ..	6.4	3.7
PF00785	1/1	93	120 ..	1	28 [.	16.2	0.006
CE00367	1/1	467	516 ..	92	142 ..	30.3	5.1e-08
PF00914	1/1	500	526 ..	1	28 [.	34.2	1.4e-08